

Fig. 1



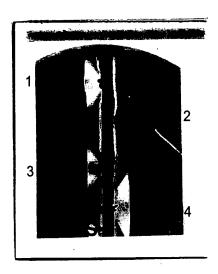


Fig. 2



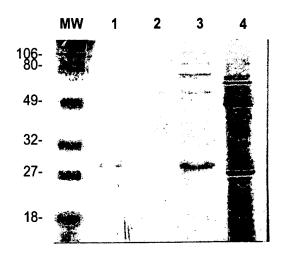


Fig. 3A

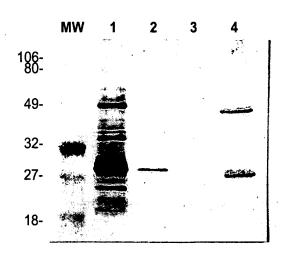


Fig. 3B



AATGAACATAAAATAAATTAATATATATTTTTTATGATAATCACATATAT <u>TTGAC</u> -35	09
TTAAAAAAATTGTTACTG $\overline{\text{TATGA}}$ TACAGGCATAAGTACTTATTTATTATAGATTGCAA $\overline{\text{-10}}$ .	120
TTTATAAACAATTATATTTTCA <u>AAGAGGAATGCTT</u> ATG GAA TTC AAA AAG TTA CTT TAT SD Met Glu Phe Lys Lys Leu Leu Tyr>	180 8
TTA ACT GGT TCA ATC GCA GGA ATT ACT TTA TTT TCC CCA ATT TTA ACA AGT GTC CAA GCA Leu Thr Gly Ser Ile Ala Gly Ile Thr Leu Phe Ser Pro Ile Leu Thr Ser Val Gln Ala>a_a_a_a_a_a_a_a_a_a_a_a_a_a_a_a_a_	240 28
AAT CAA ATA AAT GTT AGT CAA CCA TCT AAT AAT GAA AGT AAT GTT ATT TCA CAG AAA AAA Asn Gln Ile Asn Val Ser Gln Pro Ser Asn Asn Glu Ser Asn Val Ile Ser Gln Lys Lys> bbbbbbMATURE PEPTIDE_bbbbbbbbb	300 48
GAA GAA ATT GAT AAT AGT CTA AAT CAG GAA AGT GCT CAA CTA TAT GCC TTG AAA GAA GAT Glu Glu Ile Asp Asn Ser Leu Asn Gln Glu Ser Ala Gln Leu Tyr Ala Leu Lys Glu Asp> b_b_b_b_b_b_b_b_mATURE PEPTIDE_b_b_b_b_b_b_b_b_b_b_	360 68
GTT AAA GGA ACT GAG AAA GAA CAA TCA GTT AAT TCA GCA ATT TCA GCT GTT GAA AAT TTA Val Lys Gly Thr Glu Lys Glu Gln Ser Val Asn Ser Ala Ile Ser Ala Val Glu Asn Leu> b b b b b MATURE PEPTIDE b b b b b b b b	420 88

# Fig. 4A



480	540	600	660	720	780	840
108	128	148	168	188		228
AAA ACT TCA CTT AGA GCT AAT CCT GAA ACA ATT TAT GAT TTA AAT TCG ATT GGA ACA AGA Lys Thr Ser Leu Arg Ala Asn Pro Glu Thr Ile Tyr Asp Leu Asn Ser Ile Gly Thr Arg>bbbbbb MATURE PEPTIDE_bbbbbb	GTA GAA GCA ATC TCT GAC GTG ATT CAA GCA ATT GTT TTT TCA ACG CAA CAG TTA ACA AAT Val Glu Ala Ile Ser Asp Val Ile Gln Ala Ile Val Phe Ser Thr Gln Gln Leu Thr Asn> ————————————————————————————————————	AAA GTT GAT CAA GCT CAC ATT GAT ATG GGA TTT GCT ATT ACG AAA TTA CTT ATT CGC ATT Lys Val Asp Gln Ala His Ile Asp Met Gly Phe Ala Ile Thr Lys Leu Leu Ile Arg Ile> bbbbbbMATURE PEPTIDE_bbbbbbbbb	GCA GAC CCA TTT GCT TCA AAT GAA TCC ATT AAA GGG CAA GTC GAA GCT GTT AAA CAA GTG Ala Asp Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly Gln Val Glu Ala Val Lys Gln Val> 	CAA GCG ACT GTG CTT ACC TAT CCC GAT TTG CAG CCT ACG GAT AGA GCA ACT ATT TAC GTT GIN Ala Thr Val Leu Thr Tyr Pro Asp Leu Gln Pro Thr Asp Arg Ala Thr Ile Tyr Val>    D	AAA TCA AAA TTA GAC AAG CTT ATT TGG CAA ACA AGA ATT ACC AGA GAT CAA AAA GTT CTT Lys Ser Lys Leu Asp Lys Leu Ile Trp Gln Thr Arg Ile Thr Arg Asp Gln Lys Val Leu>           b         b         b         b         b         c	AAT GTA AAG AGT TTT GAA GTT TAT CAT CAA TTA AAT AAA GCT ATC ACA CAT GCA GTA GGT Asn Val Lys Ser Phe Glu Val Tyr His Gln Leu Asn Lys Ala Ile Thr His Ala Val Gly>

# Fig. 4B



GTA CAA TTA AAT CCA ACT GTA ACA GTT GCA CAA GTT GAC CAA GAA ATC AAA GTG CTA CAA Val Gln Leu Asn Pro Thr Val Thr Val Ala Gln Val Asp Gln Glu Ile Lys Val Leu Gln> bbbb MATURE PEPTIDE_bbbbbbbb	900 248
GAA GCA TTA AAT ACT GCT CTA CAG TAAGGTAGAGATTGAATTGA	960 256
GGAATTTATTAATTTCAGTCCTTTAGAATTTTTATTTAGCTGATTTACTTGTTGAAGAGA	1020
TTTGGTGGAAAATCAAGTACCATACTTCATTTCTCCTCCAAATACTTGTATGTCGATTCC	1080
CTTCTAAAACATAGCTAATTAGTTTTCTGGCTAATAGATTGTACATGAAATTGTT	1140
CAAAATTACTAGGGTAAAAGGTTTTTTTTTTTTATAAATTCATGACTAT	1190

## Fig.4C



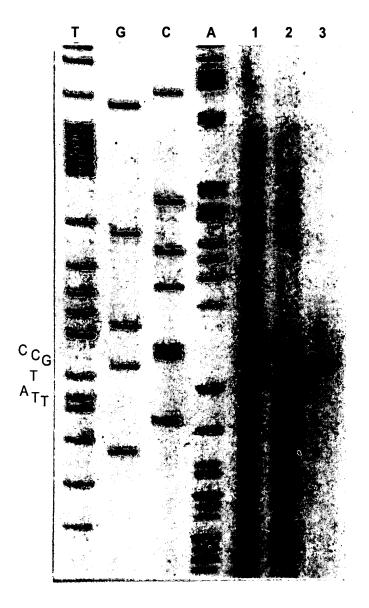


Fig. 5



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SUCAMP
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                                     ::: .. ..
                               :. :
SAGCAMP
                               DQVTTPQVVNHVNSNNQAQQMA -22
SUCAMP
       - QKKEEIDNSLNQESAQLYALKEDVKGTEKEQSVNSAISAVENLKTSLRAN -95
        SAGCAMP
       - QKL-----DQDSIQLRNIKDNVQGTDYEKPVNEAITSVEKLKTSLRAN -65
SUCAMP
       - PETIYDLNSIGTRVEAISDVIQAIVFSTQQLTNKVDQAHIDMGFAITKLL -145
         SAGCAMP
       - SETVYDLNSIGSRVEALTDVIEAITFSTQHLANKVSQANIDMGFGITKLV -115
SUCAMP
       - IRIADPFASNESIKGQVEAVKQVQATVLTYPDLQPTDRATIYVKSKLDKL -195
        SAGCAMP
       - IRILDPFASVDSIKAQVNDVKALEQKVLTYPDLKPTDRATIYTKSKLDKE -165
       - IWQTRITRDQKVLNVKSFEVYHQLNKAITHAVGVQLNPTVTVAQVDQEIK -245
SUCAMP
         SAGCAMP
       - IWNTRFTRDKKVLNVKEFKVYNTLNKAITHAVGVQLNPNVTVQQVDQEIV -215
       - VLQEALNTALQ -256
SUCAMP
         :: :::::
SAGCAMP
       - TLQAALQTALK -226
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Fig. 6



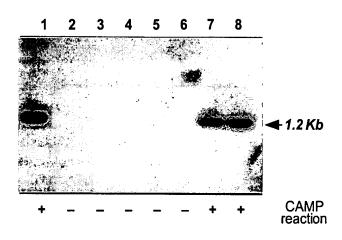


Fig. 7



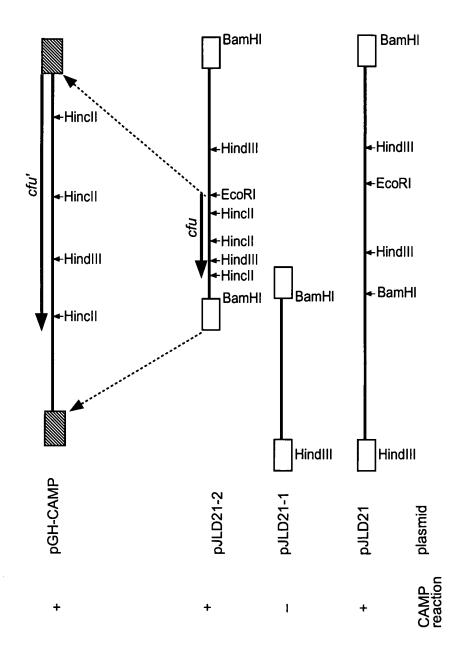


Fig. 8

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